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Exhibit 2: Alignment of Xenopus APC (Query) with Human APC (Subject)

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gb|AAA60353.1| UG polyposis locus-encoded protein
Length=2844
Score = 1360 bits (3520), Expect = 0.0, Method: Composition-based stats.
 Identities = 747/861 (86%), Positives = 797/861 (92%), Gaps = 6/861 (0%)
           MAAASYDOLVKQVEALTMENTNLRQELEDNSNHLTKLETEATNMKEVLKQLQGSIEDEAM
Query 1
           MAAASYDQL+KQVEAL MEN+NLRQELEDNSNHLTKLETEA+NMKEVLKQLQGSIEDEAM
           MAAASYDOLLKOVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM 60
Sbjct 1
           ASSGPIDLLERFKDLNLDSSNIPAGKARPKMSMRSYGSREGSLSGHSGECSPVPVGSFOR 120
Ouerv 61
           ASSG IDLLER K+LNLDSSN P K R KMS+RSYGSREGS+S SGECSPVP+GSF R
           ASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR 120
Sbjct 61
Ouery 121 RGLLNGSRESAGYMEELEKERLLIAEHEKEEKEKRWYYAQLQNLTKRIDSLPLTENFSM 180
            RG +NGSRES GY+EELEKER LL+A+ +KEEKEK WYYAQLQNLTKRIDSLPLTENFS+
           RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL
                                                                        180
      121
Query 181 QTDMTRRQLEYEARQIRAAMEEQLGTCQDMEKRVQTRVGKIHQIEEEILRIROLLOSOVA
            QTD+TRRQLEYEARQIR AMEEQLGTCQDMEKR Q R+ +I QIE++ILRIRQLLQSQ
Sbict 181 OTDLTRROLEYEAROIRVAMEEOLGTCODMEKRAQRRIARIQQIEKDILRIRQLLQSQAT
                                                                       240
Query 241 EAAERTPQSKHDAGSRDAEKLPDGQGTSEITASGNVGSGQGSSSRADHDTTSVMSSNSTY 300
            EA ER+ Q+KH+ GS DAE+ +GQG EI + + G+GQGS++R DH+T SV+SS+ST+
Sbjct 241 EA-ERSSONKHETGSHDAERQNEGQGVGEINMATS-GNGQGSTTRMDHETASVLSSSSTH
                                                                        298
Ouery 301 SVPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCIAMRQSGCLPLLIQ 360
            S PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCI+MRQSGCLPLLIQ
Sbict 299 SAPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQ 358
Ouerv 361 LLHGNDKDSVLLGNSRGSKEARASGSAALDNIIHSQPDDKRGRREIRVLHLLEOIRAYCE
                                                                        420
            LLHGNDKDSVLLGNSRGSKEARA SAAL NIIHSOPDDKRGRREIRVLHLLEOIRAYCE
Sbjct 359 LLHGNDKDSVLLGNSRGSKEARARASAALHNIIHSOPDDKRGRREIRVLHLLEQIRAYCE 418
Query 421 TCWEWQEAHEQGMDQDKNPMPAPVDHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAEL
            TCWEWQEAHE GMDQDKNPMPAPV+HQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAEL
                                                                        478
           TCWEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAEL
Sbjct 419
Ouery 481 LOVDCEMYGLINDHYSVTLRRYAGMALTNLTFGDVANKATLCSMKSCMRALVAQLKSESE 540
            LOVDCEMYGL NDHYS+TLRRYAGMALTNLTFGDVANKATLCSMK CMRALVAOLKSESE
      479 LOVDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESE 538
Sbict
      541 DLOOVIASVLRNLSWRADVNSKKTLREVGSVKALMECALDVKKESTLKSVLSALWNLSAH 600
Ouerv
            DLOOVTASVLRNLSWRADVNSKKTLREVGSVKALMECAL+VKKESTLKSVLSALWNLSAH
      539 DLOOVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAH 598
Sbjct
Query 601 CTENKADICSVDGALAFLVSTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRE 660
            CTENKADIC+VDGALAFLV TLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRE
Sbjct 599 CTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRE 658
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Query	661	NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNAKDQBGLWDMGAVSMLKNLIHSKHKMI NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARN KDQE LWDMGAVSMLKNLIHSKHKMI	720
Sbjct	659	NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSKHKMI	718
Query	721	AMGSAAALRNLMANRPAKYKDANIMSPGSSVPSLHVRKQKALEAELDAQHLSETFDNIDN AMGSAAALRNLMANRPAKYKDANIMSPGSS+PSLHVRKQKALEAELDAQHLSETFDNIDN	780
Sbjct	719	AMGSAAALRNLMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDN	778
Query	781	LSPKTTHRNKQRHKQNLCSEYALDSSRHDDSICRSDNFSIGNLTVLSPYINTTVLPGSSS LSPK +HR+KQRHKQ+L +Y D++RHDD+ RSDNF+ GN+TVLSPY+NTTVLP SSS	840
Sbjct	779	LSPKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSS	836
Query	841	PRPTMDGSRPEKDRERTAG 859	

R ++D SR EKDR ER G Sbjct 837 SRGSLDSSRSEKDRSLERERG 857

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